

SEQ ID NO:16

Rat Smooth Muscle Myosin Heavy Chain Gene Sequence (-4,216 to +11,795)

Nucleotide 1 corresponds to -4,216 bp relative to the SM-MHC transcription start site

5' Sub
10
15
20
25
30
35
40
45
50
55

AGATCTTAAA	ACACATCAAC	CTGGGCTGAG	GGGATGTGTG	TCTCTGTGTC	TGTGTATGCA	60
CATGCATTTG	AGGCCAGATG	AAAAATGTCAG	ATGTCCTCTC	ACTGCTTTAT	TCCCTTGAGA	120
CAGGGTCCCT	CACTGAACCT	GTTGGAGCTA	TGCTGGTAGC	CAGCAAGCCC	CAGTGGCCTT	180
CCTGTCTCTA	TCTCACACAG	CACAATATGT	GTGGCCATGC	TCCACTTTTT	TACATGGAAA	240
TTGGGGTCTT	CCAACTGGGG	TTCTCATTTG	TGCAGTGACA	CTCTTCCCCA	CTGAGCCATC	300
TCCTCAGGCC	AGCTGATATA	TTTTTAAATA	ATTAAATATT	TAGCACATGC	CTTTAGAAGC	360
CAATAGCTAT	TTAAAGCTGT	TTGCTTAAAA	AAAAAAAAAA	AAAAAAGACT	TCATTATCCC	420
AACACTTATG	AGGGAGAGAC	AATAATTCCA	AAACCAGAAC	CAGCCAGGGT	ACACAGTGAG	480
ACTTTATTTA	AAAAAAAAAA	AAAAAGAAAG	AAAGAAAAAA	AAAAGAAAAA	GAAAAAATAA	540
GGCTCCAAAG	AGAAATTTCC	CCTTCATCAT	CTAATCACAA	GAAAACAATT	TATTTATTTT	600
GACATCACTC	AGTCCAAAGG	AGCTTTTTGT	AAAGTGACTT	CTCTTCTTAA	AATAAGTGAC	660
CCTTCCCAAC	CACCAAAAAA	AAAAACAGAA	CCTCTGCCCT	GTTCTAGAGT	CCTTTTGAAG	720
ACTTCAGATA	CCTGAAGAGT	GGACAGATAT	TTACCGAGTG	ACTTAAATGA	ACATACTGTC	780
CCTGGGTAAT	GCTCAAGCAT	GCCAGGAGAG	CATGGATGGT	TTATGCAAGG	CTGGCACTGT	840
CATTAACAAC	TCAGTAAGGC	GGAGAAGACA	GAGAGCCTCT	CCTAAGACAA	TGGCACATAA	900
GGACATGGGT	AACCCAGAG	GTTCCCGGCT	AGTACTTAGC	AGAGCTGAGA	TCAGACTTGG	960
GCCTCTGTGC	TCGCTTGCCT	AGTGGGCAAC	ACTCAAGACT	GGGGTAAACA	ATAAGTTGAT	1020
CTGGGATATG	GCTCAGTAAT	CACACTGAGA	ATTCAACACT	GGGAAGGCAG	AGGAGGATCC	1080
CTGGGATTGC	TGCCTGGCTC	TCTAGCAGCC	TAGCAGAATC	AACAACTCC	AGGTTTCAAGT	1140
AGAGATGCTC	ACAAAATAAA	ATGGAGGAGC	AACTGAACAC	ACTCAGTGTT	GACCCACACA	1200
CACACTAAAG	AACACGTGTA	CCACACAGAC	ACAGACACAG	GATAACCTAC	CCATGTTGTG	1260
TATGGACTCA	GCCAGCCAG	GTTGGAAACT	CAGTTCCTCT	GTTAACTCTT	TTCAAACCTG	1320
GGTCTCAGC	GATGTGCTGG	GGAACCTACT	TCACGGCATT	ATTCTGGGCA	TTAGATGTAA	1380
AGGAAGCAGT	AAAGTTTCCC	TTTTCTTGAC	TGAGGTGATG	CGAGAATGAG	GGCCTGAATT	1440
CCATCTCTAG	GACTCACATA	AAGACACCCA	GACTGCACTG	GCCAGTAAGC	CTCACCTATG	1500
CCTCCAAGCC	TGGCTGTGAG	AGACTGTCTC	AAAAACAAAG	TAAAAACAAC	AAAATCAATG	1560
TCAGATGTGC	ACACATCGAA	TCCCAGCATG	TGTACGGCAT	GCTTGAGTGC	AGCCTTGTTT	1620
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GAAGTGACAT	TTGTGACTGA	CAGATGTGCA	CATCTACCAC	ATGCACATCA	CAGTTTCCAT	1740
TTTACAAAAA	GGTTAACTACT	TACTAATTGA	TTAGGGAGTG	GGGCACCCCA	CTGCTACATG	1800
TGAAAGCCAG	AGAATGATGT	GTTCCAGTCG	GTCAAGTTGTG	TCCTTCCACC	ATGTAGGTCC	1860
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TGGGCTTCCC	TCCTTCATTC	CTCCTGGGCT	CAATGCCAAG	CCGGTTTCCA	TTCTTTTAC	2160
GTGCACTGCG	AAGAGGCTTT	GGGGAAGCGG	CCTCATCCAT	CATGCAGAGA	GCTCCTCCCC	2220
CACCTCTACA	GAGAGCCAGC	CAAGCTGCTG	TCCTTGCTC	TGCTCTGTCC	ACCCTGTGAG	2280
GAGGCTGGGA	TGAGGTTGGG	GATGGGGAGG	ATCAGGATTC	AGATGTTTTT	AAGTCTGAGA	2340
AGCAGGTGAG	CTTGGTCCTA	GAAGAATATG	GAAGGGTCT	ACTGGGGTTG	AGATATAGAT	2400
CAGTGTATCA	AAGTCAACAG	GGGGGCTGTG	TGGCTTTTTT	ATATCCCAA	GTCAGCTTGG	2460
TGCTGGTTTC	CTAGGCTTCC	TGAGTCCGAC	AAAGGTGCAG	TGTGTTAATC	TCACACCACT	2520
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GGTAACTAAG	AGCCAGTACT	TGCCCATGGT	CCTGCTGTTA	TAAAGAGGCT	CAGTAGACTC	2640
CCATTCAAAC	AACTGTGCTC	AGAGGCCTTC	TGTCGTCTCG	TGGCCAATTG	CCCTATTGCT	2700
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TCAGCTCTTC	TGGCCTGCAA	AATGGGGCTG	GGACAGGTTG	GCCAGGATCA	TCCTCTGGTT	2820
GGGAGAACCA	GCTGCACGTG	GGTCTGGAGC	TCTTATTAGT	ACTGGGGTCC	CCATAACGCT	2880
CCATGGGGCT	AGCGGGAGGC	TGCACGGGAC	CATATTTAGT	CAGGGGGAGC	CAGGCCCCCG	2940
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TCCCCGCCAG	GGCCAGGAGG	GAGGACCAAC	TCAGGACCTC	GAGGGTCCGT	GCGCGGGGAG	3060
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	CACACACAGA	GAGAGACAGA	CAGACAAAGA	GAGAGACAGA	GACAGAGAGA	CACACACAGA	3360
5	GAGACAGACA	GACAAAAAGA	GAAGAGAGAC	AGAGACTTTA	GGGACGTAAT	CATCACAGGG	3420
	AAATCAAAGC	TAAGAGTGTG	ATGAAAAGAG	TGTCAGGTCA	GACAAAAGAG	ACAGGGGCCA	3480
	AGATCCGTAC	AGGGCTAAGG	GACACAGAGA	TTGAGAACAC	CGAGTGGTAA	GGGGGGCAGC	3540
	TGACAGCAGG	TCCCCCACAT	TCTCTTAGAG	TCTTAGCATG	CATCCTCCAA	GTGCCATAAC	3600
10	GCAGTAGCAA	CCCCGCTTTT	AACGATGCTC	AGAGAAACCA	TGTTATTGGT	CCCAGGCACC	3660
	CCGGTTGTAG	GGTGAAAAGG	GCTGCAGAGA	ACAAGTTGGA	AAAACAAGTT	TCCCAGCAGT	3720
	CACAGAGGAT	ATGCAGTGAC	TGTGCCGACT	TGTTTTTTTT	TTTTTAAGTC	CCCTTCCCCC	3780
	CCCCCGCCCC	GCCCCCGGCT	TGCTAAGCAC	AACCGGCTTC	GAATCTTAGG	AAGTGGCAGG	3840
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15	AAGAGGTTAA	AATCCAGCTG	GAATGGACCT	AGGGGAAGAA	ATTCTCAAGT	CTCCCTACAG	3960
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	CAGAGGCTCT	GTTCTCACC	TGCAGGGGGC	GCTGGGAAGG	GCAGAGGACC	CTCCACCCCC	4140
	GCCCCGCAGT	CACCTCCCCT	TCCCCACCTT	CGGGTAGCGC	TGACTCTATA	AAGCCAGATG	4200
			transcription start site +1				
20	TCCGAAGCAT	ACAGAGAGAT	TTGGACCATC	CCAGCCTGGG	ATCAGTGTCA	GATCCGAGCT	4260
	CTCCATCCGG	TGTTCTCCTG	CTAGTCCACC	CCAGTAGCAG	ATCTGTAAGT	AGAAGTTGAT	4320
	CCCTTAGGGG	CAAGCCTGGG	CGGTGAGCTT	GAGCAGCTTC	TAAAACATCC	TCCAGGGAGT	4380
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25	CAGGACCACC	CTAGACCTCC	CGTGATTACT	CCCATCTCTC	GCACCAAACC	AGCATCCTCA	4500
	GGTTGCCTAT	GAACAGAACC	ACCTGGGAAA	GTGGGGTAGG	TAATTAAAGG	TTCTGGCCAC	4560
	TGGGCCCAAT	TCCAGGTATT	TTAAGACTAC	AGTCTAAAAA	GCAAACAAAA	TGGCCTACTT	4620
	AAAAACTAAC	TAGTGACACA	GTGGACAAGT	GAAGTGTGGT	GGAAACTGTG	GGTCTGAATT	4680
	CAAATACCAG	TATTGAAAAT	AATAAGAAGT	CTGGGATAAA	TATCCACTGA	ACATCCCCAG	4740
30	AATACTCAAA	ACATGGGTTA	AAGTTTAATG	ACTCTGAACA	CAGGCCGTGT	GTTCTTATTC	4800
	CACTCCTAAT	GGAATGTGCT	GTTGAAAATT	TACTGGTAAA	CAAAAATGCT	TAATGTTAAA	4860
	TAAGGTCTGT	TCTTCCTCTG	TTACTTCCAA	AACACAAATC	TCCATTAAAA	AGGAACCTTC	4920
	TCCAGTTTGG	TTGGGCCCCC	AGATGCCGCG	GTGGGTGCTG	AGGCTCCATT	TGCATCCCCC	4980
35	ACACTGAGTG	AGCAGACGAT	GGATTTTGGG	GCTCCTCAGT	GGGAAGGTTA	CTCTCAGGTC	5040
	AGGGAGAGGA	GCTAGCAGAG	AAATTTATGC	TATTCAGTTT	CAGAATTGGA	GAAGTCTTGC	5100
	CATGTCCAGA	AAGCACCTTT	CAAAGTTATG	TCTGTCAGAG	AACAGAAAAA	TTTTTTTTTGA	5160
	AAGCCAGGAC	AAGGCTGCTT	TGGTTCTACT	ACTAAGAACT	GAAAAACTGC	TGACTTGCTG	5220
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40	GAAAGTCTCT	CATAACAAGA	AACACTTTCT	CTTTTATGAT	GTTGTTGATG	GCACACTTAA	5400
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	CTTACCTTGT	CTTGACATCT	CTGTTTTTCC	CAAAACCAAA	ATTTGTTGGA	CTCCTGTTTC	5520
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45	ACCAATTTAA	AATGACAGAG	ACTGTCTTTT	AAATTTTGTT	GATGTTGTTG	TTTCCCTGTG	5640
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	ATGGTAGTGT	TTTCTATGAG	GCCATTCCCA	GTCCCCCTTG	GCCAATCACC	CAGCCTTTTC	5880
	ATGCAGCCTG	ACTGGCTTGA	GTTCTGGGTA	CTTCTCTGTC	TTTCCCTGTA	GAGATGGACA	5940
50	ATGAAGTTCT	TTTTTTCCTC	TCTTTTCTTG	TTTGGAAGTT	CTATTTGTAT	TTTTTTGGTG	6000
	GAAATTATAT	TCCACATATC	TAATAAGAAC	GGGTGGTGTT	TACATCTAAT	AAACATTGA	6060
	ATAATTTTGA	AACAGGATAA	AGACGATCTT	TTTAGAAAAA	TATATCCCGT	TTCAAATACT	6120
	CAGAATCAGG	TCTTAACCAC	ATTATTTTGC	CAGGTATGGT	GGCTTGTGTC	TAAAATACTA	6180
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55	GCCATCCTGG	ACTACAGTGG	GAAACACTAT	CTTGGAAGAA	ATAAAAAATA	AAAATCAAAA	6300
	CCCAGCCTAA	TGGTACATAA	CTTCAATTCC	AGCATCTGAG	GTAAACCAGG	AAGCACAGCT	6360
	GATTAATGAA	CCCAAAGTCA	GCCTGGGCTA	CCTAAGGAAT	CCTATCTTTT	ACAATTTGTT	6420
	GATGCTGTTG	TCATTTTCTT	GATCACTTTC	CCATCTGCAG	AATGGGACTG	TTGAGAACAG	6480
	CCAGCGTGTT	AATGTTTCTG	TAGCACTTGC	TTAGTCTTCT	GAGAAGTAGA	AGATCACTTA	6540
	GCTAGGGTTT	GATCCCCATG	ACTGCAGCAA	AAGAGGAAGA	CTCATTAATT	GGAGTCTTCA	6600

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	GAGCCTAATG	CCCTTTTGGG	AGCTTTCAAT	AGATAACCCA	TGTGAAGGGT	CTGACACAAG	6780
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5	GAGCATATTC	TGTATGACAC	AGCTGATATC	AAGAAACCCA	AACGGTGGCC	TTTCCCCTAA	6900
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10	GCACTGTAGC	AAGGGGAGGT	CAGGCTACCA	TGATGCTCCT	GCGCTTCAGG	GAATTATCCT	7140
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	CAGCATAAGA	ACTATGTCTG	CCAACCTGCG	AGGGGAAGTT	GCTCAAGATG	CTATGCAAAC	7380
	ACTCCAGCTT	TCCATGGAAG	GGACTTCAGC	ATCTATGGAT	GGTGGTAGCA	AAGCACTCCT	7440
15	CAAGCTGATC	AAAGAATAGC	TGTCCTTTCC	TGCCCCCTCC	CTAATGAAGC	GTGCAGTCAG	7500
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	CACCCATCTG	TGAGCACAAA	TCTTGATATT	TCACCTTTGC	TTTATACAGA	TGTTTGTATA	8340
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35	CTTAGCACCT	ATTTTAAACA	TTGTTCTACC	TGAGTTGTAA	GATGCAAAAC	ATAGTGGGGC	8700
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40	CCTAGATCTC	TTTCCCCTCC	ACTCTAACGT	TACAACATAC	AGCTCTCTCT	CTCTCTCTCT	9000
	CTCTCTCTCT	CTCTCTCTCT	CTCTCTCTCT	CTCATTTTAT	TTTTTAAAAA	AAATTTTATT	9060
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	TTGCTGGGAA	TTGAACTCAG	GACCTCTGGG	AGAGCAGTCA	GTACTCTTAA	TGCTGAGCCA	9240
45	TCTCTCTAGC	CCTTTCCCCC	TCTTCTAAAA	CATAGTTTTT	GAAGATCTAA	CGCAGATCTT	9300
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	GTTATTGTGA	TGGGACAAGT	TCTTATTCTC	TTTCTTCTGA	GGAGGTACCC	TGGAGACCTT	9540
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	TTGGGTATCT	TCTAACTGGG	TGGTGGTGGT	ACATGCCTGT	AGTCCCAGCT	CCTGGGAGGC	15960
40	AGAGGCAAGT	AGATCCGAAT	TCTCGCCCTA	TAGTGAGTCG	TATTAGTCGA	C	16011
						+11,795 (1st intron)	

SEQ ID NO:17

The 5' (-5086) and 3' limits of the Human SM-MHC Promoter-Enhancer LacZ Transgene Tested in Transgenic Mice

5 The number in the left margin refers to the position within an undefined BAC sequence contained in the public database (Accession # U91323 in GenBank). The start site (i.e. +1 position) of the SM-MHC gene corresponds to the BAC position 143,590.

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 147661 GACATATTCA GATGTGTCAA ACATCGCTAA TGCCATCTCT GAGTAAATTA GGCTTCAAAC
 147721 AGATCGGGAT TCTAATCCTG GTTCCCCAAC TTTTGCAAGG GAGGGCCTTG CATTTACCTT
 147781 TCAAGACCCC GATAGGCTTA GCAGGAAAAA GGAATAATA GATAATGCCA CTCTTTCATC
 147841 CTTGGACTTT TTGTCTAATT ATATGAATTT ATCTGTAGGA TAAATTTCCA GAAATGCGCT
 147901 TGCTGAGTTA AAGGGCATGC GTATCTAAAA TTAATAGATA TTGCAAATGA CTGGCTAAAG
 147961 ACATTGCAGA CCAGGTGCAG TGGCTCACGC CTGTAATCCC AGCACTTTTG AGCCCGCAG
 148021 CAGGTGGGTC ACCTGAGGTC AGGAGTTCAA GACCAGCCTG GCCAACATGG TCTCTGCTAA
 148081 ACCCTATCTC TACTAAAAAT ACAAAAAATTA TCTGGGCATG GTCGTGGGCA CCTGTAATCC
 148141 CAGCTACTCG GGAGGCTGAG GCACGAGAAT CGCTTGAGCC TCAGAGGCAG AGGTTGCATT
 148201 GAGCCGAGAT CACACCACTG CACTCCAGCC TGGGCAAAGA GTGAGACTCG GTCTCAAAAA
 148261 AAAAAAAAAA AAGGCATTGC AAATTGCAAC TTGTTGCAGT CACATATGAC AGCAGTCCCC
 148321 ATCCTCTTGG CACCAGAGAC TGGTTTCGTG GAAGACAATA TTTTCCAGGG TGGAGTGGGG
 148381 AGGATGGTTT TGGGATGAAA CTGTCCCACC TCATCATCAG GCATTGGTTA GATTCTCATA
 148441 AGGAACGTAC AACCTAGATC CCTTGCAGGT GGAGTTGGCA ATAGGGTTTG TGCTTCTGTG

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148501	AAAATCTAAT	GCTGCTTATC	TGACAGGAGG	CGGAGCTTAG	GCAGTGATGG	TCACTCACCC
148561	ACCGTCCCCT	CCTGCTATGT	GGCCTGGTTC	CTAACAGGCC	ATTGACTGAT	ACTGCAGCAC
148621	AAGGGTTGGG	GACCCCTGAC	ATAGGAGACT	ATACATTTAT	TTTAAGCTGT	GGTATGCCAG
148681	AATTGTAAAA	TATAAACAC	AGTGGGGCTT	TTAGGGCCAG	AAATAATCAG	TTCTTGCTCG
148741	CTTCCAGAAAG	CATCCTTCAC	AGGGGCTACC	GTAACCTCTG	CCAACCAAGT	TCTCTTGTTT
148801	GGGAGGAAAA	AATAGTGTTA	TGCATTAAGA	GAACCTCTTT	CTGGAGTTAC	TTGAAACCAT
148861	TGGTATTTCAG	ATGATTAGGC	AGATGTCACA	AGGCAATAAG	AATGTGACAG	GTTCCACCATT
148921	CACTTTTTTT	CCTGTAAAAG	TGAAGTAGGG	CTTTCTTGCG	AACAAGCCCT	TGGGAGGTGG
148981	GGGGATGTGA	ATGGTGAGGG	GAGGGTAGAA	ATGGTGAGGT	AGGGTCAGGG	GCAAGAAAGG
149041	GACTTTCTGC	TAAGAATTAA	TCGGGTGTCC	ATTTACTCTT	AGCAGAAAAC	TAGGATTAGA
149101	TTCTGGATTG	TACTCCTGAC	TCCAAATTTT	ACAAGTGGGG	GTCTTGCAAT	TACCTTCCAG
149161	GACCTCGGTC	ATCTTAGCAG	GAAAAATAGCA	ATAGCAGGTG	ATGCCACCTT	ACAGAGCGCT
149221	TAGGAGACAG	TGAGATGGTC	TATATAGGAA	CTGTCTGGC	CTGATACCTG	ATGAATACAA
149281	GGGGCCCAAT	AAATACAGTG	GCTGTTATGA	ATAATAGATC	TAAACTGCCT	TTTTGGTACT
149341	ACTGGGGACC	TGCCAAGCAG	GTGCATTTAG	AGTGCCCACT	GCCTCTCCCT	GCGACACATT
149401	TGATGCCTCC	CTACACCTGG	ACCAGGCCCT	GAGCGAGGAT	TTCCACTGCA	GAGGTCTTTC
149461	CAGCTGGCGA	ATTGTGTTGC	AGATCAGGTT	CAGAGAACTT	CTGTTTTGCC	TGTGTGGCAT
149521	TCATTCAATC	GTTTATTTGA	AATAGAGATG	GGATCTCACT	GTGCTGCCCA	GGCTAGTCTA
149581	GAGCTCCTAA	TTCAAGCAAT	CCTCTTGGCT	TGGCCTCCCA	TAGTTCTTGG	ATTACAGGTG
149641	TGAACCACTG	TATCCAGCCC	TTTATGACAT	TTAGAATATG	AGCAATTTTT	CTTTTTTCTT
149701	TTTTTTCTTT	TTGAGATGGA	GTCTCACTCT	GTCAACCCAGG	CTAGAGTGCA	GTGGCATGAT
149761	CTTGGCTCAC	TGCAACCTCT	ACCTCCCAGG	CTCAAGCGAT	CTTCCCACCT	CAGCCTCCCC
149821	AGTAGCTGGG	ACTACCGGCA	TGTGCTGCCA	TGCCTGGCTA	ATTTTTGTAT	TTTCTGTAGA
149881	GATGGGGTTT	CACCATGTTG	CGCAGGCTGG	TGTCAAACCT	CTAAGCTCAA	GCGAAGTGGC
149941	TGCCTTGGCC	TCCCAGTGTT	GGGATTACAG	ACGTGAGCCA	CAGTGCTGAA	CCCTGCATGG
150001	TATTTAGAAAT	ATAAGCAATA	CTCTAACATC	TGGTCTGGGT	CACCTCTGTAT	TACTTACCTG
150061	ATCTCCAAAA	ACATTTGGGT	TTTTGTCTCT	GGTCCAAAAT	CTTTAGCCAA	TGGCTTGGCA
150121	GTAAAATCCT	GAGGGAAGCT	GTTGACCAGG	TGAGGTGATG	TGCAAATCCT	ATACTCTCTG
150181	GGCTCTGGGA	TATTTAATTT	ACTATTTATT	TATTTATTTT	CAAGACAGAG	TTTTTGCTCTT
150241	GTGCGCCAGG	CTGGAGTGCA	GTGATGGGAT	CTCAGCTCAC	TGCACCCCTC	ACCTCCTGGG
150301	TTCAAGCGAT	TCTCCTTCCT	CAGCCTCCTG	AGTAGCTGGT	ATTACAGGCG	CCCACCACCA
150361	CACCTGGCTA	TTTTTTGTAT	TTTTAGTAGA	GACGGGGTTT	CACCATGTTG	GCCAGGCTGG
150421	TCTTGAACCTA	CTGACCTCAG	GTTATCCGCC	TGCCCTCGGC	TCCCGAAGTA	CTGGGATTAC
150481	AGGCATCAGC	CACCATGCCC	GGCCTAATTT	ACTTTTTTATT	AATGCTGAAAG	CAGAGAGGGC
150541	AAGATCTTTT	GCCCCTGAGT	TCTTCTGGGA	AAAATGAAAC	TGATGGTAAA	ACAAACTAAA
150601	GCAACCTGAC	ATTCTCAGTT	GGTCCAGTTT	CAGCCCTTTG	ACTGGGAGTC	ACAGACGGGT
150661	CCCATAAAAT	GGTAGAGCTG	GGCCAGCCTA	CCATTGATTT	ATTTTCCCTA	AATGAAAAAT
150721	ACAAGGCCCA	GAGAGGGCAA	GTGACTTGTC	CAGAGTCACC	CAGCAGGTTT	GGGGCAAAGC
150781	TGAGACTCGT	TACTTGACAT	CCTAAGGTCT	TCCAGAGGCT	AATGATTAGC	TTGTTTGTGC
150841	TCAAAAAATG	AAGCAGCCTG	GGCGCGGTGG	CTCATGCTTG	TAATCCTAGC	ACTTTGGGAG
150901	GCTGAGGCAG	GCAGATCGCT	TGAGCTCAGG	AGTTTGAGAC	CAGCCTGGGC	CACAAAGTGA
150961	GACCCCTGTC	TCTACAAAAA	AATGCAAGAA	TTAAAAAATT	AGCTGGGTGT	TCTGGTGCGT
151021	GCCTGTGATC	CCAGCTACTT	GGGAGGCTGA	GGTGGGAGAA	TGGCTTGAGC	CTGGGAGGCA
151081	GAGTTTGCAG	AAAGCAGAGA	TCGCGCCACT	TCACTCTAGC	CTGGGCAACA	GAGCCAGACC
151141	CTGTCTCAAA	AAAAAAGAAT	GAAGCAGTTG	TTGGTCAGGA	CAGGACTGTA	AACAAGGCTG
151201	ACACACTCAG	ATGTGTCAAA	CATCGCTAAT	GCCAAAGGTG	ACAGAGTCAT	TTGTTTTTCAT
151261	CCAAACATTC	GAGAAAGTTG	GACGAGGTGA	CTCACGCCCT	TCATCCTAGA	GCTTTGGGAA
151321	GCCAAGGCAG	GAGGATCATT	TGAGATCAGG	AGTTTGAGAC	CAGCCTAGGC	AAAATAGCAA
151381	GACCCCATC	TCTACAAAAA	ATAAGCCGGG	CATAGTGGCC	CACACCTGAG	GTGGGAGGAT
151441	CCCTTGAGCC	CATGAGTTTG	AGCCTGCAGT	AAGCTATGAT	TGCACCAGTC	CACCTCCACCC
151501	TGGGCATATA	GTGAGACCTT	TCCCCAACCC	AAAAACATTG	AGAGCAGCTC	TTGATGAGTG
151561	AACGTGACTT	CGTGGTCAGC	AGTTCTGGGT	AGTAATTTCA	GAGATGTCCT	TTCAGCCCTT
151621	GGAGCTGATG	CAGGACCTTA	AACATGAGCG	ATGGTGAGAG	AGGGAGGGTT	GGGAAGGTGC
151681	ATCAAGGTAG	ATGAAGAGTG	TCCCTGGGGT	TGGGCCAACT	GGCGGTCCGT	CTCTGGTCCA
151741	GTGTGTTTAC	CTTGCCCCCG	TCTGATCTTC	TGCAGTTGGT	ATTCCGAGTT	GAGTTTGAAT
151801	AAGTGAGAGC	TGCTCTCAGC	TTTAACTGCC	TTTCCCAAGA	CAGCCCTTGT	TTTTATTCTA
151861	AAGCTGTGGT	TCTCAACTGG	AAGCAGTTTT	GCCACCCAG	GGGACATCTA	GCAGTGTCTG
151921	GAGACATTTT	TGATTGTTCAT	GAGTGAGGGA	AGGGGTGCTA	CTGGCATCAG	GTGGGCAGAG
151981	ACCAGGGATG	CTGCGGAACA	TCCCACAATG	CACGGAAGAG	CTCCCCCTAC	GACACAGAAT

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152041	GACGCAGCCC	AAGAGTCACA	GTGCAGAGTT	TGTGGCCAGC	TGCGGTGGCT	CACGCCTGTA
152101	ATCCCAGCAC	TTTGGGGGGC	CAAGGTGGGA	GGATTGCTTG	AGGCCTGGAG	TTCAAGACCA
152161	GCCTGGCCAA	TATGGTGAAA	CCTCATCTCT	ACTAAAAATA	CAAAAATTAG	CCAGGCATGG
152221	TAGCGCATGC	CTGTAGTCCC	AGCTACTTGG	GAGGCTGAGG	CACGAGAATC	ACTTGAACCC
152281	AGAAACGTGG	AGGTTGCAGT	GAGCTGAGAT	TGCGTCACTG	CACCTCCAGCC	TGGGTAACAG
152341	AGCGAGACTC	TGTGTCAAAA	AAAAAAAAAA	AAAAAAAAAGA	CTTAGCAACT	ATTATTACTA
152401	GTATTAGTAT	TATTAATTTG	TCAGGCTCAC	TGAATTTTCT	CAAAAATTTG	GCAAATTTTT
152461	AGGAAAACAT	TCTCAAAACA	TTTGGCAAAT	CTGTGGCTAA	ATGTTGTTTT	GGGGACCCAA
152521	GGCTCGTAGG	AGCAAAACAG	CTTTCAGGTT	TCCGGATCTG	CCAGAGACTC	AAGTGTCTCTG
152581	TTGTGTGTTT	TGTGTCTCAA	TGAGGGAAAG	GGGAATATGT	AGCACCTTCC	AGATGGATTT
152641	GACCTTGACT	GCGCCACTGT	TTGAAGAGCT	TCTCAACCTC	CGCAGCTCCA	CCCCAGCCCA
152701	GATATTTTCA	GGAATTAGGG	TTCCAAGGGG	CATGCTATGG	AAAACACCAT	TCTAGCATGA
152761	GTGGAAGCTT	CTCATCCCCC	ATCTTGCTGT	CTTTTGACCA	AAGCAGATTT	TGCACGTCTGT
152821	AACTGTCTAGA	GACATCAAAAG	CCAGAGGGAA	TCCAGCCTGC	TCCAAGCTCT	CCTTTTTTGT
152881	ACAGAGACTG	AATCTTTTGA	CTTGATCTTG	TTTGTGTTTT	TAAGTCTGAG	GTTAGACAGG
152941	GTCCCAGGCA	ATGGAGGCGT	GCGTGTCTCT	TTATTTTTCT	GTTGTAGCTT	TTGCTATTTT
153001	TTCTGACTTT	TAAGGCAACT	CATCCACATG	GCAATTAGGA	AGAGCCCACT	TAGGGCTGGG
153061	CACAGCGGCT	CATGCCTGTA	ATCCCAGCAC	TTTGGGAGAC	CGAGGCAGGC	AGATCACTTG
153121	AGGTCAGGAG	TTCAAGACCT	CAGCCTGGAC	AACATGGTGA	AACCCCGTCT	CTACAAAGAA
153181	TACAGGAAAA	TAGCTGGGCA	TGGTGGCAGG	TGCCTGTGGT	CCCAACTATT	TGGGAGGCTG
153241	GGGTGGGAGG	ATCACTTGAG	CCTGGGAGGC	GGAGGTTGCC	GTGAGCTGAG	GTGATGCCAC
153301	TGCACTCCAG	CCTGGGCGAC	AGAGCAAGAC	CCTGTCTCAG	AAAAAAAAAA	AAAAAAAAAA
153361	GAAGTCCACT	TTACTTGTC	TAGTGCTTAG	AACAAATGAA	ACACTCTCCT	AGCCCTCTTG
153421	GGATGTAATT	GGCTACCATC	TGCACAAACT	CTTCATTATT	GCACAAGAAT	ATCAATATAC
153481	TTAATGCTAC	TGAACTGTGT	TTAAGTGGCC	GAGGTGGTGA	ATGTTAGCTG	TATTTTACCA
153541	CAATTAAAGA	TAAGAGGGAA	GGAAAATGAA	GTGTACTTTA	CAACCAAAAA	AGTACGCTTG
153601	ATGTGCAAAA	AAGTGTGCAG	CTTGATGAAT	TTTCAAGAGG	ATATATTTTT	TATAGATGGG
153661	GGTCTCACTC	TGTCACCCAG	GCTGCAGTGC	AGTGGCATGA	TCATGGCTCA	CTGCATCCCC
153721	GACCTCCTGA	GCTTAAGTGA	TCCTCCCACC	TCAGCCTCCT	GAGTAGCTGG	GAAGTGCAGG
153781	GCACACTATC	ACAACCGGTT	AATTTTTTGT	TGTTTGCTAG	AGACAAGGTT	TCACCATGTT
153841	GACCAGGCCG	GTCTCAGCCT	CCTGGGCTCA	GGTTATCCTC	CTACCTCAGT	CTTCCACACA
153901	GGTAATTAAA	AAACATTTTT	TCTTAGAGAT	GGGTCTTGCT	GTGTTGGCCA	GGCTGGTCTC
153961	AAACTCCTGG	GCTCAAGTGG	TCCTCCCATC	TGGGCTTCTC	AAAGTGTCTG	GATTACAGGC
154021	GTGAGCCATG	TCACCTGGCC	CAACAGTTTG	ATGAATTTTC	AGAAAGTGAA	CACCTCATAGG
154081	GCTGGCATTG	AGATGAAGAT	CTAGAGGTCA	ACCCCTCACA	GCCCCCTCA	CGTTCTGTCC
154141	TTGCAATCAT	TGCACACCGG	AGACTCATTC	ATTCCTTATC	TGAGTTCTAT	CACCGTAGAT
154201	TAATTCTGCC	TGGTTTTTGA	CCTCAGTTCA	ATAGTCACAG	AACCTGTGCT	TTTTGTGACC
154261	ACCTTCTTTT	GCTCAAGGAT	GTGTTGTGAG	ATGTCCTTTT	TTGTGGTGTG	GAGCTGTAGT
154321	TTACTTCACC	TGATTTCGAGT	CCTATTTTGG	GTGTTTGTA	TGTGTCAGGT	ACTGTGCCAG
154381	GTGCCTTACA	GGATTGATTG	CTTTATGGGC	ATCTGACAAG	CCCACCCACC	TTATGTGAAA
154441	GGCAGAACCA	AATAGACTCC	AGAATGAGAC	CCAGGTTTGG	GTCCCAGCTC	TGACACTTCT
154501	TTTTTTTTTG	GATGGAGGCT	GACTCTGTCC	CCAAGGCTGG	AGTGTAGTGG	TATGATGTCTG
154561	GCTTACGGCA	ACCTCCACCT	CCCGGGTTCA	ATGATTCTC	CTGACTCAGC	CTCCCAAGTA
154621	GCTGGGGCTA	CAGGCACGTA	CCACCAATCC	TGGCTAATTT	TTAATTTTTG	TATTTTTAGT
154681	AGAGACAGGG	TTTCACAATG	TTGGCCAAGC	TGGTCTCAAA	CTCCTGACCT	CAAGTTATCC
154741	TCCCACCTCA	GCCTCCCAAA	GTTCTGGGAT	TATAGGCATG	AGCCATCACA	CTCGGCCTAC
154801	TTGTGATCAA	TCTTACTTCA	TCTTCACACC	CTCCCATTTT	TCTTACGCAT	CCTCCAGTTT
154861	CTCTCTCTCT	CTCTCTCTCT	TTTTCTCTCT	CTCTCTCTCA	CACACACACA	CACGATCTGC
154921	TGCGACACCT	TAAGAAACAA	GAGATTATCA	GGGAATGATT	GAATATTTTG	CCGCATTTCC
154981	TATTTTGCTG	CCTGTTTAAA	CTAACCTTGG	TTATACTATT	AAAAGAAGAC	GCGTCGTATC
155041	AAGCCACTTC	TGTGACTATG	GCTGCTCAGA	AATAAACATA	ATTAAACAT	CCAACGTAG
155101	TAAATGCTAT	TGGTTAGGAA	TGAGCGAAGT	GGCTTAGAGT	CACCGGAAGT	GAGAAAGGGT
155161	ATAGAAACAG	AAGGTACTTG	GTGTAGATCA	GGGGTGTCTT	ATCTTTTGGC	TTCCCTGGGC
155221	CACCCAGAAA	AAAGAAGAAT	TGTCTTGGGC	CACACGTAAA	ATACACTAGC	ACTAATGATA
155281	GCTGATGAGC	TAAAAAATA	AAAAAAATC	GCGAAAAAAT	ATCATACTGT	TTTAAGAAAG
155341	TTTATGAATT	TGTATCGGGC	CACATTCAAA	GCCGTCCTGG	GCCCCATGCA	GCCTGTGGGC
155401	TGCAGGTTAG	ACAAGCTTGG	TGTAGAGAGT	TTCATCTAAA	CTTCATGGCA	GCTCTGCAGG
155461	GCACCCGTTA	GGTCCCCAGT	ATTAATATAC	AGTAAATCTG	AGTCTCAGAT	CTACGTAAGT
155521	CACCCAGAAG	CACGCATTCT	GCAGTGGCAG	AGTCACGTTT	GAATTAGCAT	CTGATTGCAA

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155581 AGTCTGGGTG TCTTTACATG ACTACAGGTT ATCTTACCTC TCAAGAGGAG GCAACCAATC
155641 AAATGTTGCC AGCACCAATG AACTTGTACT TTATTTAGGC TCAGAAAGAT CTTTtaggct
155701 AATGAAAATG CCCTATATTT ATGAAATGTT CTCGTTCTCT GTGGCTTTCT CTTTTTTGAG
155761 ACAGGGTCTC ACCCTGACAC CCAGGCTGGA GTGCAGTGAT GTAATCATAG CTCACATGAG
155821 CCTCAAACTC CTGGGCTCAA GCAACCCTCC TGCCTCAGCC TCCTAGTAGC TGGGACTACA
155881 AGCACGCATC ATCATGCCTG GCTGATATTT TTTTAAAGGG ATGGGGTCTT GCTATAATGC
155941 CCAGTCTGGT CTCGAACTCC TGGGCTCAAG CAATCCTCCT GCCTTGGCCT CCAAAATAT
156001 GGGATTATAC ATGTGGGCTA CTGCCAGCCT CTTTTCTTTC AATTATTTTT TAATCTATGG
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156121 GTGGCTCACA CCTGTAATGT CAGCACTTTG AGAGGCCAAG GCCGGTAGAT CACCTGAGGT
156181 CAGGAGTTTG AGACCAGCCT GGACAATATG GTGAAACCCC GTCTCTACTA AAAATACAAA
156241 AATCAGCCAG GCGTGGTGGC ATGCACCTGT AATCCTAGCT CCTCGGGAGG CTGAGGCAGG
156301 AGAATCACTT GAACCTAGGA GGTGGAGGTT GCAGTGAGCC AAGATCCCGC CATTGCACTC
156361 TAGCTGGGCG ACAGAGCATA GTCTCTCACC TTTGGGAGTT TACTGCATTG TTTAGCATGC
156421 TCTCCTGTGC CTTGCATTTT CCATAGACAG GCGTCAGATC TGGAGGCTTC ATCACCTTCA
156481 TCCCCATCT CCATCCCCTT TTCTTTTGAG CAAGAATATG TCATTAGTGG TAACGGCACT
156541 TCCTGTAGTG GCCCATCTGC AGGCATGTAA TGTTTATAAT GTCTAGTCAG CTCTCTCTTT
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156661 ATTCCACAAG AGCTCTTCAT CTGATATAGT CAGTCTTGTT GTGGGGACCC TAGACCAGCA
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156841 ATTACTGGTA GAACTTGCCA ACTTGCCAAG ACCCTTCTTT TCTTCCTTTC TTTCTTTTTT
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